

MULTIPLE ALIGNMENT:

52180312	-----	
A1237625	-----	
SPKinaseinHSDA59H18	PKHLLVFINPFGGKGQGGKRIYERKVAPLFTLASITTDIIGNKFYVYVEVITEHANQAKE	
52180312	-----	
A1237625	-----	
SPKinaseinHSDA59H18	TLYEINIDKYDGI VCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA	
52180312	-----	
A1237625	-----	
SPKinaseinHSDA59H18	GSTDCVCYSTVGTSDAETSA LHI VVGDSLAMDVSSVHHNSTLLRYSVSLG YGYGDI I K	
52180312	-----	
A1237625	-----	
SPKinaseinHSDA59H18	DSEKKRWLGLARYDFSG LK TFLSHHCYEGTVSFLPAQHTVGS PRDRKPC RAGCFVCRQSK	
52180312	-----	
A1237625	-----	
SPKinaseinHSDA59H18	QQL EEEQKKALYGLEAAEDVEEWQVCGKFLA I N A T N M S C A C R R S P R G L S P A A H L G D G S S	
52180312	-----	
A1237625	-----	
SPKinaseinHSDA59H18	DL I L I R K C S R E N F L R I R H T N Q D Q D F T F V E V Y R V K K F Q T S K H V E D D N D L K E I L E K Q	
52180312	-----	
A1237625	-----	
SPKinaseinHSDA59H18	KFGK I C K D R P S C I T S A S R S S W N C D G E V M H S P A T E V R V H C O L V R L F A R G I E E S	
52180312	-----	
A1237625	-----	
SPKinaseinHSDA59H18	R F G H I C S S H P S C C C I V S N S S W N C D G E V L H S P A I E V R V H C O L V R L F A R G I E E N P K P D S H S	

FIG. 2

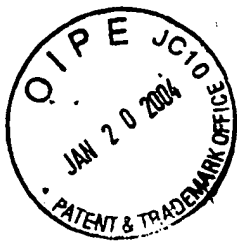


FIG. 3A
FIG. 3B

FIG. 3

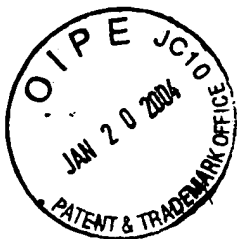
FIG. 3A

SPkinaseinHSDA59H18	-----MEKPY-----AFTVHCVKRAERERWKWAQVT	C1
corrected_human_sphingosine	-----MDPAGGRGVLPKPC-RVLEVLINPRGGKGKALQLEFR	
AF068748_EXT-2	-----MEFEVCPGRLLPKPC-RVLEVLINPQGGKGKALQLEFO	
Q06147	LYIDYDPHSS-SHLDDEE---DDLVEEILKRSYKNTRRNK-SIEVLEINPFGGKGKAKLTFM	
Q12246	LLIDHVSRSKRANTGEENISSGTVEEIEIKSYENSKRNR-SIEVLEINPFGGKGKAKLTFM	
Q14159	CWDFVENSDF-----QFCEYLLDVAYKGIKRSR-RFLVLEINPFGGKGKAKLTFM	
Q18425	CRSDAEENEQ-----LTSVILSRKPPPOEQCRGNLEVFANPNSGKSKSLETEFA	
SPkinaseinHSDA59H18	FWCPPEQLCH-----LWLQTLREMLEKLTSPK-HLEVFANPFGGKGKAKLTFM	
corrected_human_sphingosine	SHVOPLEAABATISFTLMILTER-----RNHARELVN---SEELGRMDALVMSGDGLM	C2
AF068748_EXT-2	SRVOPLEAABATISFTLMILTER-----KNHARELVC---ABEIGHMDALVMSGDGLM	
Q06147	TKAKPILLASRCSTIEVNTKY-----PGHAIEIAR---EMDIDKYDTTACASGDGIP	
Q12246	TKAKPILLASRCSTIEVNTKY-----ARHAIDIAK---DLDISKYDTTACASGDGIP	
Q14159	SEAEVFSSEHSICIEVNTKY-----KDHADSHAK---NLDSVESMDGILLSVGGDGIF	
Q18425	NTVGPDKDSLRYEVVVTG-----PNHARNVLMT---KADLEKFNGLVILSGDGLV	
SPkinaseinHSDA59H18	RKVAPLFTLSHTIDIGNKFYVNVYVEVITEHANOAKETLYETINIDKYDEGIVCVGGDMF	
corrected_human_sphingosine	HEAVNGIMERPD---METAIQKPLCSIPACSCNATAAASINHYAGVEQVITNEDLLTNCHTEL	C3
AF068748_EXT-2	HEAVNGIMERPD---METAIQKPLCSIPGSGGNAIAASVNHYPAGVEQVITNEDLLTNCHTEL	
Q06147	HEVINGIYQRPD---VKAFNNITAITETPCGSGNAMSVS---CHWITN---NPSYSTLELITK	
Q12246	YEVINGIYRPPD---VDAFNKLAVTQLPCGSGNAMSIS---CHWITN---NPSYAALGLVK	
Q14159	HEVINGIGERDD---YLEAFKILFVCMIPGSGGNAFSSYN---AIG---OLKPALEALEIEK	
Q18425	FEALINGITCRD---ERIFPTLFIIGIVPSSGNGILCSVLSKYGIKMKNEKSVMERALEIFA	
SPkinaseinHSDA59H18	SEVLFGEIDGRTQRSAGVDQNGPRAVIMFSSLRIGIIPAGSTDCVCYSTVGTSDAETSALH	
corrected_human_sphingosine	LCRPVLSPMNILLSLHTASGLRSFMSLSIAGGFIADVDLESCKNR-REGEMRFTLGTFIRI	C4
AF068748_EXT-2	LCRRRISPMNILLSLHTASGLRLMSLSISMGFVADVDLESEKVR-REGEIFRTMGTEFRI	
Q06147	SIEFTRIDLCCSQPSYAREHPKI-SFELSOTYGLIAETIDINTEFIR-WMEPARFELGVAFNI	
Q12246	SIEFTRIDLCCSQPSYMWNPRI-SFELSOTYGMIAESDINTEFIR-WMEPVREN LGVAFNI	
Q14159	GRPTSFKLMTFEQ---KGGKALSFITANYCHTADCDIGIENWR-FMEENRAYLGFFIRL	
Q18425	TSPTEAKAESVALYSKTDNQSYA-SFELSIGMGLMADIDIDSEKMRKSLGHRFTVMGEIRS	
SPkinaseinHSDA59H18	IVVGDSLANVDVSSVHHNSTLLRMSVSLIGYGFYGDIIKDSEKVR-MGLARYDFSGLKTFF	



C5

coorected_human_sphingosine AF068748_EXT-2 Q06147 Q12246 Q14159 Q18425 SPkinaseinHSDA59H18	AAALRTVRCPLATLIVRVGF-----KTP----- ASLRITVQCCLAYLVEIVTAS-----KRP----- IQKKKYPCEIYVKYAAKSKNEIKNHYLEHKNKGSLEFQHTMKNKDNECDNYYENEYET IQKKKYPCEVFKYAAKSKKEIKVHFLNKDK-----NKGCLTFE-PNPSPN EQKPDWKCSTIEMDVSSDRTEIKHMYE--KSK----- CNLRSTVKCPITVRYDKPKGFHPSSNVFSVEK-----TTQQRID-- LSHHCYEGTVSFLPAQHTVGSFRD-----RKP-----CRAGCFVCR--
coorected_human_sphingosine AF068748_EXT-2 Q06147 Q12246 Q14159 Q18425 SPkinaseinHSDA59H18	-----ASPVVVQQ-----GFVDAHLVPLPEEQ-MPSHWQVWP--D -----ASTIAQK-----GHVDTHLVPLPEEP-MPSHWITVWP--E ENEDEDADADDESHLTSRDADSSADQ-IKEEDFKIKYPLDEG-IPSDWERLDPNIS SSPDLLSKNNINNSTKDELSPNFLN-----EDNFKLKYVMTPE-MPRDWEKMDSELT -----N-----LAPMSES-----SDSKTVSTSPPE--SHLLTFE--I -DSKVKTNGSVSDSEETMETKFN-----WTIPDSDDETAVG-SSDLEETV--IE QSKQQLBEEQKKALYGLEAAEDVEEWQVCGKFLATNATNMSCACRRS[ER]GLSPAAGLGD
coorected_human_sphingosine AF068748_EXT-2 Q06147 Q12246 Q14159 Q18425 SPkinaseinHSDA59H18	EDFVLIALLSHLSLSEMFAPMGRCAAGMWHIFYVRAQVSRAMLLRLFLAMEKGRHMEY QDFVLVLVLLHHLSSSELFAAPMGRCEAGMWHIFYVRAQVSRAMLLRLFLAMEKGRHMEY NNLGLFYTGKMPYADTKFFPAALPSDCTMDWITLARTSLTRMAPILGLDKC--SHV DNLTIFYTGKMPYADTKFFPAALPSDCTMDWITLARTSLTRMAPILGLDKC--SHV NDLSLFCAGLLPYIAPDAKMFPAASNDGLIDMVLVYSKQTEKSLLSMFTQDNG--GFY DNFVNITYAVTLSHIAADGPFAPSAKLEBNRIHLSYLLWKDIGTRUNIAYILLAIEGETH GSSDLJLIRKCSRNFRLIRHTNQDQDFTFVEVYRVKQFQTSKIMED[ED]SDLKEG
coorected_human_sphingosine AF068748_EXT-2 Q06147 Q12246 Q14159 Q18425 SPkinaseinHSDA59H18	ECPLYLVVVPVVAFRLEPKDGK-----VFAVDGELMVSEAVQGOVHBNYFVMVSGCVEPPPS DCPLYLVVVPVVAFRLEPRSQRC-----VFSVDGELMVCEAVQGOVHBNYLMVCGSRDAPSG LQPEVHLSKLLAYKHPKICNG-----LFSVDGEEKFPLEPLQVETIMPRICKTLR----- LEPEVHLSKLLAYKHPKIVESC-----LFSVDGEEKFPLEPLQVETIMPRICKTLR----- YSKHINYYKVRSEFTBHNITCKRHYEALDGESYPLEPPEECRABKIGTTLSP-----V DL[EF]VKHVEVSSMKLEVISSEGS--HVLLDGEVDTKTTEVASTKNHISVFSSTA----- GKKRFCHICSSHPSCCCTMSNS--SNODGEVLIHSPATEVRTHQCVRLFAR-----
coorected_human_sphingosine AF068748_EXT-2 Q06147 Q12246 Q14159 Q18425 SPkinaseinHSDA59H18	WKPQQMPPPPPEPPL RDSRRGPPPEEP- -NGRYVDTDFDSM -NGRYVDTDFDSM AGFQLLDI----- -GIEENPKPDSHS



PHYLIP - PROTEIN DISTANCE ANALYSIS

SEQUENCES ANALYZED:

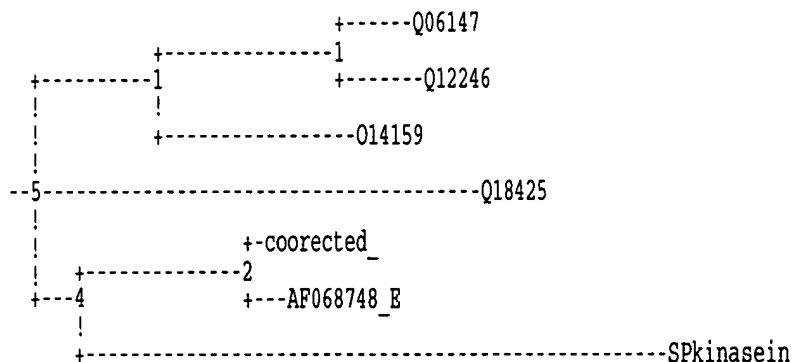
1. SPkinaseinHSDA59H18
2. Q18425
3. O14159
4. Q06147
5. Q12246
6. coorrected_human_sphingosine
7. AF068748_EXT-2

7 POPULATIONS

NEIGHBOR-JOINING/UPGMA METHOD VERSION 3.572c

NEIGHBOR-JOINING METHOD

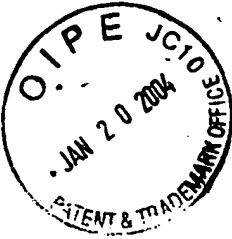
NEIGHBOR BRANCH LENGTHS ALLOWED



REMEMBER: THIS IS AN UNROOTED TREE!

BETWEEN	AND	LENGTH
5	3	1.09970
3	1	1.59865
1	Q06147	0.79847
1	Q12246	1.02742
3	O14159	1.74537
5	Q18425	4.00995
5	4	0.43259
4	2	1.44382
2	coorrected_	0.24774
2	AF068748_E	0.37392
4	SPkinasein	5.26443

FIG. 4



MULTIPLE ALIGNMENT:

80432911 SPkinaseinHSDA59H18	ACAPGADACSVPVSEI.IAVEETDVHGKHQSGKWKQMEKPYAFTVHCVKRARRHRWKWAO -----MEKPYAFTVHCVKRARRHRWKWAO
80432911 SPkinaseinHSDA59H18	VTFWCPPEEQ LCHLWLQTLREM LKLT SRPKHL L VFINPFGGKGQKRIYERKVAPLETLA VTFWCPPEEQ LCHLWLQTLREM LKLT SRPKHL L VFINPFGGKGQKRIYERKVAPLETLA
80432911 SPkinaseinHSDA59H18	SITTDIT I-----VTEHANOAKETLYEINIKDVGIVCVGGDMFSEVLHGLIGR SITTDITIGNKFVYVNYVEVITTEHANOAKETLYEINIKDVGIVCVGGDMFSEVLHGLIGR
80432911 SPkinaseinHSDA59H18	TORSAGVDONHPR----- TORSAGVDONHPRAVLVPSSLRIGITPAGSTDCVCYSTVGTSDAETSALHIVVGD SLAMD
80432911 SPkinaseinHSDA59H18	VSSVHHNSTLLRYSVSLGYGYGDIKDSEKKRWLG LARVDFSG LKTF LSHHCYEGTVS -----
80432911 SPkinaseinHSDA59H18	FLIPAQHTVGSPRDRKPCRAGCFVCRQSKQQL EEEQKKALYGLEAAEDVEEWQVVC GKFLA -----
80432911 SPkinaseinHSDA59H18	INATNMSCACRRSPRGLSPAHLGDGSSDLILIRKCSRNF LRLIRHTNQDQDFDFTFV -----
80432911 SPkinaseinHSDA59H18	EVYRVKKFQETSKHMEDESD LKEGKKRFCHTCS SHPSCCCTVSNSSWNCDEVLHSPA -----
80432911 SPkinaseinHSDA59H18	IEVRVHCQLVRLFARGIEENPKPDSHS -----

FIG. 5